

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANTS: Chatterjee, Deb K.
Solus, Joseph
Yang, Shuwei
- (ii) TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
Nucleic Acid Fragments and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 93
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
(B) STREET: 1100 New York Ave., N.W., Suite 600
(C) CITY: Washington
15 (D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
20 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: (To be assigned)
25 (B) FILING DATE: 06-FEB-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: (To be assigned)
(B) FILING DATE: 06-JAN-1998
(C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/037,393
(B) FILING DATE: 07-FEB-1997
(C) CLASSIFICATION:
- 35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0942.4250002
- (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2682 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGAGAC TATTTCTCTT TGATGGCACA GCCCTGGCCT ACAGGGCATA TTACGCCCTC 60
 GACAGATCCC TTCCACATC CACAGGAATT CCAACGAACG CCGTCTATGG CGTTGCCAGG 120
 10 ATGCTCGTTA AATTCATTAA GGAACACATT ATACCCGAAA AGGACTACGC GGCTGTGGCC 180
 TTCGACAAGA AGGCAGCGAC GTTCAGACAC AACTGCTCG TAAGCGACAA GGCGCAAAGG 240
 CCAAAGACTC CGGCTCTTCT AGTTCAGCAG CTACCTTACA TCAAGCGGCT GATAGAAGCT 300
 CTTGGTTTCA AAGTGCTGGA GCTGGAGGGA TACGAAGCAG ACGATATCAT CGCCACGCTT 360
 GCAGTCAGGG CTGCACGTTT TTTGATGAGA TTTTCATTAA TAACCGGTGA CAAGGATATG 420
 15 CTTCAACTTG TAAACGAGAA GATAAAGGTC TGGAGAATCG TCAAGGGGAT ATCGGATCTT 480
 GAGCTTTACG ATTCGAAAAA GGTGAAAGAA AGATACGGTG TGAACACACA TCAGATACCG 540
 GATCTTCTAG CACTGACGGG AGACGACATA GACAACATTC CCGGTGTAAC GGAATAGGT 600
 GAAAAGACCG CTGTACAGCT TCTCGGCAAG TATAGAAATC TTGAATACAT TCTGGAGCAT 660
 GCCCGTGAAC TCCCCAGAG AGTGAGAAAG GCTCTCTTGA GAGACAGGGA AGTTGCCATC 720
 20 CTCAGTAAAA AACTTGCAAC TCTGGTGACG AACGCACCTG TTGAAGTGGA CTGGGAAGAG 780
 ATGAAATACA GAGGATACGA CAAGAGAAAA CTACTTCCGA TATTGAAAGA ACTGGAGTTT 840
 GCTTCCATCA TGAAGGAACT TCAACTGTAC GAAGAAGCAG AACCCACCGG ATACGAAATC 900
 GTGAAGGATC ATAAGACCTT CGAAGATCTC ATCGAAAAGC TGAAGGAGGT TCCATCTTTT 960
 GCCCTGGACC TTGAAACGTC CTCCCTTGAC CCGTTCAACT GTGAGATAGT CGGCATCTCC 1020
 25 GTGTCGTTCA AACCAGAAAAC AGCTTATTAC ATTCCACTTC ATCACAGAAA CGCCCAGAAT 1080
 CTTGATGAAA CACTGGTGCT GTCGAAGTTG AAAGAGATCC TCGAAGACCC GTCTTCGAAG 1140
 ATTGTGGGTC AGAACCTGAA GTACGACTAC AAGGTTCTTA TGGTAAAGGG TATATCGCCA 1200
 GTTTATCCGC ATTTTGACAC GATGATAGCT GCATATTTGC TGGAGCCAAA CGAGAAAAAA 1260
 TTCAATCTCG AAGATCTGTC TTTGAAATTT CTCGGATACA AAATGACGTC TTATCAGGAA 1320

CTGATGTCGT TTTCCTCACC ACTTTTGGT TTCAGCTTTG CGGATGTTCC GGTAGACAAG 1380
GCTGCGAACT ACTCCTGCGA GGATGCAGAC ATCACTTATA GGCTCTACAA GATACTCAGC 1440
ATGAAGCTCC ATGAAGCGGA ACTTGAGAAC GTCTTCTACA GGATAGAGAT GCCGTTGGTG 1500
AACGTTCTTG CACGCATGGA ATTGAACGGG GTGTATGTGG ACACAGAATT CCTGAAAAAG 1560
5 CTCTCGGAGG AGTACGGCAA AAAGCTCGAG GAACTGGCCG AAAAAATCTA CCAGATAGCA 1620
GGTGAGCCCT TCAACATCAA TTCTCCAAAA CAGGTTTCAA AGATCCTTTT TGAGAAGCTG 1680
GGAATAAAAC CCCGTGGAAA AACGACAAAA ACAGGAGAGT ACTCTACCAG GATAGAGGTG 1740
TTGGAAGAGA TAGCGAATGA GCACGAGATA GTACCCCTCA TTCTCGAGTA CAGAAAGATC 1800
CAGAAACTGA AATCGACCTA CATAGACACC CTTCCGAAAC TTGTGAACCC GAAAACCGGA 1860
10 AGAATTCATG CATCTTTCCA CCAGACGGGT ACCGCCACTG GCAGGTTGAG TAGCAGTGAT 1920
CCAAATCTTC AGAATCTTCC GACAAAGAGC GAAGAGGGAA AAGAAATTAG AAAAGCGATT 1980
GTGCCCCAGG ATCCAGACTG GTGGATCGTC AGTGCGGATT ATTCCCAAAT AGAACTCAGA 2040
ATCCTCGCTC ATCTCAGTGG TGATGAGAAC CTTGTGAAGG CCTTCGAGGA GGGCATCGAT 2100
GTGCACACCT TGA CTGCCTC CAGGATCTAC AACGTAAAGC CAGAAGAAGT GAACGAAGAA 2160
15 ATGCGACGGG TTGGAAGAT GGTGAACTTC TCTATAATAT ACGGTGTCAC ACCGTACGGT 2220
CTTTCTGTGA GACTTGGAAT ACCGGTTAAA GAAGCAGAAA AGATGATTAT CAGCTATTTT 2280
ACACTGTATC CAAAGGTGCG AAGCTACATC CAGCAGGTTG TTGCAGAGGC AAAAGAGAAG 2340
GGCTACGTCA GGACTCTCTT TGGAAGAAAA AGAGATATTC CCCAGCTCAT GGCAAGGGAC 2400
AAGAACACCC AGTCCGAAGG CGAAAGAATC GCAATAAACA CCCCATTCA GGAACGGCG 2460
20 GCAGATATAA TAAAATTGGC TATGATAGAT ATAGACGAGG AGCTGAGAAA AAGAAACATG 2520
AAATCCAGAA TGATCATTCA GGTTCATGAC GAACTGGTCT TCGAGGTTCC CGATGAGGAA 2580
AAAGAAGAAC TAGTTGATCT GGTGAAGAAC AAAATGACAA ATGTGGTGAA ACTCTCTGTG 2640
CCTCTTGAGG TTGACATAAG CATCGGAAAA AGCTGGTCTT GA 2682

(2) INFORMATION FOR SEQ ID NO:2:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 893 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ala	Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala	
	1				5					10					15		
5	Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr	
				20					25					30			
	Asn	Ala	Val	Tyr	Gly	Val	Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Lys	Glu	
			35					40					45				
10	His	Ile	Ile	Pro	Glu	Lys	Asp	Tyr	Ala	Ala	Val	Ala	Phe	Asp	Lys	Lys	
		50					55					60					
	Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Val	Ser	Asp	Lys	Ala	Gln	Arg	
	65					70					75					80	
	Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg	
					85					90					95		
15	Leu	Ile	Glu	Ala	Leu	Gly	Phe	Lys	Val	Leu	Glu	Leu	Glu	Gly	Tyr	Glu	
				100					105					110			
	Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Arg	Ala	Ala	Arg	Phe	Leu	
			115					120					125				
20	Met	Arg	Phe	Ser	Leu	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val	
		130					135					140					
	Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu	
	145					150					155					160	
	Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro	
				165						170					175		
25	His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Asp	Ile	Asp	Asn	
				180					185						190		
	Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu	
			195					200						205			
30	Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Tyr	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu	
		210					215					220					
	Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile	
	225					230					235					240	
	Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val	
				245						250					255		

Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu	
		260						265			270					
Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln	
		275						280			285					
Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	Ile	Val	Lys	Asp	His	
		290			295						300					
Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	Glu	Val	Pro	Ser	Phe	
305					310						315			320		
Ala	Leu	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asn	Cys	Glu	Ile	
		325						330						335		
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	Ala	Tyr	Tyr	Ile	Pro	
		340						345						350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Thr	Leu	Val	Leu	Ser	
		355						360			365					
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln	
370					375						380					
Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Ile	Ser	Pro	
385					390						395			400		
Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro	
		405						410						415		
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly	
		420						425			430					
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu	
		435						440			445					
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Asn	Tyr	
450					455						460					
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser	
465					470						475			480		
Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu	
		485						490						495		
Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr	
		500						505						510		
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys	
		515						520						525		
Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	
530					535						540					
Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu	

35

His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
 850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880

5 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Leu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu
 1 5 10 15

Leu Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu
 20 25 30

Val Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg
 35 40 45

Gly Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe
 50 55 60

Ala Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr
 65 70 75 80

25 Gly Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu
 85 90 95

Lys Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser
 100 105 110

30 Leu Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys
 115 120 125

Pro Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn
 130 135 140

Leu Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp
 145 150 155 160

Pro Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val
165 170 175

Leu Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met
180 185 190

5 Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu
195 200 205

Asp Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu
210 215 220

10 Leu Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val
225 230 235 240

Pro Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr
245 250 255

Tyr Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu
260 265 270

15 Glu Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala
275 280 285

Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys
290 295 300

20 Leu Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile
305 310 315 320

Tyr Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val
325 330 335

Ser Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr
340 345 350

25 Thr Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile
355 360 365

Ala Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile
370 375 380

30 Gln Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn
385 390 395 400

Pro Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala
405 410 415

Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Leu Pro Thr
420 425 430

35 Lys Ser Glu Glu Gly Lys Glu Ile Arg Lys Ala Ile Val Pro Gln Asp
435 440 445

Pro Asp Trp Trp Ile Val Ser Ala Asp Tyr Ser Gln Ile Glu Leu Arg

T02290-222660

	450	455	460
	Ile Leu Ala His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu 465	470	475 480
5	Glu Gly Ile Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val 485	490	495
	Lys Pro Glu Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val 500	505	510
	Asn Phe Ser Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg 515	520	525
10	Leu Gly Ile Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe 530	535	540
	Thr Leu Tyr Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu 545	550	555 560
15	Ala Lys Glu Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp 565	570	575
	Ile Pro Gln Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu 580	585	590
	Arg Ile Ala Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile 595	600	605
20	Lys Leu Ala Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met 610	615	620
	Lys Ser Arg Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val 625	630	635 640
25	Pro Asp Glu Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met 645	650	655
	Thr Asn Val Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile 660	665	670
	Gly Lys Ser Trp Ser 675		

30 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 610 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Lys	Glu	Leu	Gln	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	
	1				5					10					15		
5	Ile	Val	Lys	Asp	His	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	
				20					25					30			
	Glu	Val	Pro	Ser	Phe	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	
			35					40					45				
	Phe	Asn	Cys	Glu	Ile	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	
		50					55					60					
10	Ala	Tyr	Tyr	Ile	Pro	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	
	65					70				75					80		
	Thr	Leu	Val	Leu	Ser	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	
					85				90						95		
15	Lys	Ile	Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	
				100					105					110			
	Lys	Gly	Ile	Ser	Pro	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	
			115					120					125				
	Tyr	Leu	Leu	Glu	Pro	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	
		130					135					140					
20	Leu	Lys	Phe	Leu	Gly	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	
	145					150					155				160		
	Phe	Ser	Ser	Pro	Leu	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	
					165				170						175		
25	Lys	Ala	Ala	Asn	Tyr	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	
				180					185					190			
	Tyr	Lys	Ile	Leu	Ser	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	
			195				200						205				
	Phe	Tyr	Arg	Ile	Glu	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	
		210				215						220					
30	Leu	Asn	Gly	Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	
	225					230					235				240		
	Glu	Tyr	Gly	Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	
					245					250					255		
35	Ala	Gly	Glu	Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	
				260				265						270			
	Leu	Phe	Glu	Lys	Leu	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	

	275						280						285					
	Gly	Glu	Tyr	Ser	Thr	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu		
	290						295					300						
5	His	Glu	Ile	Val	Pro	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu		
	305					310					315					320		
	Lys	Ser	Thr	Tyr	Ile	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr		
				325						330					335			
	Gly	Arg	Ile	His	Ala	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg		
				340					345					350				
10	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu		
			355					360					365					
	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp		
	370						375					380						
15	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala		
	385					390					395					400		
	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile		
				405						410					415			
	Asp	Val	His	Thr	Leu	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu		
				420					425					430				
20	Glu	Val	Asn	Glu	Glu	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser		
			435					440					445					
	Ile	Ile	Tyr	Gly	Val	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile		
	450						455					460						
25	Pro	Val	Lys	Glu	Ala	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr		
	465					470					475					480		
	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu		
				485					490					495				
30	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln		
				500					505					510				
	Leu	Met	Ala	Arg	Asp	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg	Ile	Ala		
			515					520					525					
	Ile	Asn	Thr	Pro	Ile	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Leu	Ala		
	530						535					540						
35	Met	Ile	Asp	Ile	Asp	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys	Ser	Arg		
	545					550					555					560		
	Met	Ile	Ile	Gln	Val	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro	Asp	Glu		

565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val
580 585 590

Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser
595 600 605

Trp Ser
610

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Ser Ser Ser Val Pro Ile Pro Gly Val Thr Gly Ile Gly Glu
1 5 10 15

Lys Thr Ala Val Gln Leu Leu Gly Lys Tyr Arg Asn Leu Glu Tyr Ile
20 25 30

Leu Glu His Ala Arg Glu Leu Pro Gln Arg Val Arg Lys Ala Leu Leu
35 40 45

Arg Asp Arg Glu Val Ala Ile Leu Ser Lys Lys Leu Ala Thr Leu Val
50 55 60

Thr Asn Ala Pro Val Glu Val Asp Trp Glu Glu Met Lys Tyr Arg Gly
65 70 75 80

Tyr Asp Lys Arg Lys Leu Leu Pro Ile Leu Lys Glu Leu Glu Phe Ala
85 90 95

Ser Ile Met Lys Glu Leu Gln Leu Tyr Glu Glu Ala Glu Pro Thr Gly
100 105 110

Tyr Glu Ile Val Lys Asp His Lys Thr Phe Glu Asp Leu Ile Glu Lys
115 120 125

Leu Lys Glu Val Pro Ser Phe Ala Leu Ala Leu Glu Thr Ser Ser Leu
130 135 140

Asp Pro Phe Asn Cys Glu Ile Val Gly Ile Ser Val Ser Phe Lys Pro

	145		150		155		160
	Lys Thr Ala Tyr Tyr Ile Pro Leu His His Arg Asn Ala Gln Asn Leu						
		165			170		175
5	Asp Glu Thr Leu Val Leu Ser Lys Leu Lys Glu Ile Leu Glu Asp Pro						
		180		185		190	
	Ser Ser Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu						
		195		200		205	
	Met Val Lys Gly Ile Ser Pro Val Tyr Pro His Phe Asp Thr Met Ile						
		210		215		220	
10	Ala Ala Tyr Leu Leu Glu Pro Asn Glu Lys Lys Phe Asn Leu Glu Asp						
		225		230		235	240
	Leu Ser Leu Lys Phe Leu Gly Tyr Lys Met Thr Ser Tyr Gln Glu Leu						
		245		250		255	
15	Met Ser Phe Ser Ser Pro Leu Phe Gly Phe Ser Phe Ala Asp Val Pro						
		260		265		270	
	Val Asp Lys Ala Ala Asn Tyr Ser Cys Glu Asp Ala Asp Ile Thr Tyr						
		275		280		285	
	Arg Leu Tyr Lys Ile Leu Ser Met Lys Leu His Glu Ala Glu Leu Glu						
		290		295		300	
20	Asn Val Phe Tyr Arg Ile Glu Met Pro Leu Val Asn Val Leu Ala Arg						
		305		310		315	320
	Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu						
		325		330		335	
25	Ser Glu Glu Tyr Gly Lys Lys Leu Glu Glu Leu Ala Glu Lys Ile Tyr						
		340		345		350	
	Gln Ile Ala Gly Glu Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser						
		355		360		365	
	Lys Ile Leu Phe Glu Lys Leu Gly Ile Lys Pro Arg Gly Lys Thr Thr						
		370		375		380	
30	Lys Thr Gly Glu Tyr Ser Thr Arg Ile Glu Val Leu Glu Glu Ile Ala						
		385		390		395	400
	Asn Glu His Glu Ile Val Pro Leu Ile Leu Glu Tyr Arg Lys Ile Gln						
		405		410		415	
35	Lys Leu Lys Ser Thr Tyr Ile Asp Thr Leu Pro Lys Leu Val Asn Pro						
		420		425		430	
	Lys Thr Gly Arg Ile His Ala Ser Phe His Gln Thr Gly Thr Ala Thr						

		435		440		445													
		Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys		
		450						455					460						
5		Ser	Glu	Glu	Gly	Lys	Glu	Ile	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro		
		465					470					475					480		
		Asp	Trp	Trp	Ile	Val	Ser	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile		
					485					490						495			
		Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu		
				500						505					510				
10		Gly	Ile	Asp	Val	His	Thr	Leu	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys		
				515					520					525					
		Pro	Glu	Glu	Val	Asn	Glu	Glu	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn		
				530				535					540						
15		Phe	Ser	Ile	Ile	Tyr	Gly	Val	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu		
		545					550					555					560		
		Gly	Ile	Pro	Val	Lys	Glu	Ala	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr		
					565					570						575			
		Leu	Tyr	Pro	Lys	Val	Arg	Ser	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala		
				580					585						590				
20		Lys	Glu	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile		
			595					600						605					
		Pro	Gln	Leu	Met	Ala	Arg	Asp	Lys	Asn	Thr	Gln	Ser	Glu	Gly	Glu	Arg		
			610					615					620						
25		Ile	Ala	Ile	Asn	Thr	Pro	Ile	Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys		
		625					630					635					640		
		Leu	Ala	Met	Ile	Asp	Ile	Asp	Glu	Glu	Leu	Arg	Lys	Arg	Asn	Met	Lys		
				645						650						655			
		Ser	Arg	Met	Ile	Ile	Gln	Val	His	Asp	Glu	Leu	Val	Phe	Glu	Val	Pro		
				660					665						670				
30		Asp	Glu	Glu	Lys	Glu	Glu	Leu	Val	Asp	Leu	Val	Lys	Asn	Lys	Met	Thr		
			675					680						685					
		Asn	Val	Val	Lys	Leu	Ser	Val	Pro	Leu	Glu	Val	Asp	Ile	Ser	Ile	Gly		
			690					695					700						
35		Lys	Ser	Trp	Ser														
		705																	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
 1 5 10 15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
 20 25 30

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
 35 40 45

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
 50 55 60

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
 65 70 75 80

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
 85 90 95

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
 100 105 110

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
 115 120 125

Met Arg Phe Ser Leu Ile Thr Gly Ala Lys Asp Met Leu Gln Leu Val
 130 135 140

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
 145 150 155 160

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
 165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
 180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
 195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
 210 215 220

	Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile	
	225					230				235						240	
	Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val	
					245					250					255		
5	Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu	
					260				265						270		
	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln	
			275					280					285				
10	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	Ile	Val	Lys	Asp	His	
		290					295					300					
	Lys	Thr	Phe	Glu	Asp	Leu	Ile	Glu	Lys	Leu	Lys	Glu	Val	Pro	Ser	Phe	
	305					310					315					320	
	Ala	Leu	Ala	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asn	Cys	Glu	Ile	
					325					330					335		
15	Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Thr	Ala	Tyr	Tyr	Ile	Pro	
				340					345					350			
	Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Thr	Leu	Val	Leu	Ser	
			355					360					365				
20	Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Ser	Ser	Lys	Ile	Val	Gly	Gln	
	370						375					380					
	Asn	Leu	Lys	Tyr	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Ile	Ser	Pro	
	385					390					395					400	
	Val	Tyr	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro	
				405					410						415		
25	Asn	Glu	Lys	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly	
				420					425					430			
	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu	
			435				440						445				
30	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Asn	Tyr	
	450					455						460					
	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser	
	465				470					475					480		
	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile	Glu	
				485					490						495		
35	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr	
			500						505					510			

	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
	515									520							525
	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro	Phe	
	530						535					540					
5	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys	Leu	
	545					550					555					560	
	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Glu	Tyr	Ser	Thr	
					565					570					575		
10	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val	Pro	
				580					585					590			
	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	
		595						600					605				
	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His	Ala	
	610						615					620					
15	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	
	625					630					635					640	
	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu	Ile	
				645						650					655		
20	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser	Ala	
			660						665					670			
	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly	Asp	
		675						680					685				
	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr	Leu	
	690						695					700					
25	Thr	Ala	Ser	Arg	Ile	Tyr	Asn	Val	Lys	Pro	Glu	Glu	Val	Asn	Glu	Glu	
	705					710					715					720	
	Met	Arg	Arg	Val	Gly	Lys	Met	Val	Asn	Phe	Ser	Ile	Ile	Tyr	Gly	Val	
				725						730					735		
30	Thr	Pro	Tyr	Gly	Leu	Ser	Val	Arg	Leu	Gly	Ile	Pro	Val	Lys	Glu	Ala	
			740						745					750			
	Glu	Lys	Met	Ile	Ile	Ser	Tyr	Phe	Thr	Leu	Tyr	Pro	Lys	Val	Arg	Ser	
		755						760					765				
	Tyr	Ile	Gln	Gln	Val	Val	Ala	Glu	Ala	Lys	Glu	Lys	Gly	Tyr	Val	Arg	
	770						775					780					
35	Thr	Leu	Phe	Gly	Arg	Lys	Arg	Asp	Ile	Pro	Gln	Leu	Met	Ala	Arg	Asp	
	785					790					795					800	

35 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

	Asn	Glu	Lys	Phe	Asn	Leu	Glu	Asp	Leu	Ser	Leu	Lys	Phe	Leu	Gly
			420					425					430		
	Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro
		435						440					445		Leu
5	Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Asp	Lys	Ala	Ala	Asn
		450					455					460			Tyr
	Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu
	465					470					475				480
10	Met	Lys	Leu	His	Glu	Ala	Glu	Leu	Glu	Asn	Val	Phe	Tyr	Arg	Ile
					485					490					495
	Met	Pro	Leu	Val	Asn	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val
				500					505					510	Tyr
	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys
			515					520					525		Lys
15	Leu	Glu	Glu	Leu	Ala	Glu	Lys	Ile	Tyr	Gln	Ile	Ala	Gly	Glu	Pro
		530					535					540			Phe
	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Lys	Ile	Leu	Phe	Glu	Lys
	545					550					555				560
20	Gly	Ile	Lys	Pro	Arg	Gly	Lys	Thr	Thr	Lys	Thr	Gly	Glu	Tyr	Ser
					565					570					575
	Arg	Ile	Glu	Val	Leu	Glu	Glu	Ile	Ala	Asn	Glu	His	Glu	Ile	Val
				580					585					590	Pro
	Leu	Ile	Leu	Glu	Tyr	Arg	Lys	Ile	Gln	Lys	Leu	Lys	Ser	Thr	Tyr
			595					600					605		Ile
25	Asp	Thr	Leu	Pro	Lys	Leu	Val	Asn	Pro	Lys	Thr	Gly	Arg	Ile	His
		610					615					620			Ala
	Ser	Phe	His	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser
	625					630					635				640
30	Pro	Asn	Leu	Gln	Asn	Leu	Pro	Thr	Lys	Ser	Glu	Glu	Gly	Lys	Glu
					645					650					655
	Arg	Lys	Ala	Ile	Val	Pro	Gln	Asp	Pro	Asp	Trp	Trp	Ile	Val	Ser
				660					665					670	Ala
	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Leu	Ser	Gly
			675					680					685		Asp
35	Glu	Asn	Leu	Val	Lys	Ala	Phe	Glu	Glu	Gly	Ile	Asp	Val	His	Thr
		690					695					700			Leu

Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
725 730 735

5 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
755 760 765

10 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
770 775 780

Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

15 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

20 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

25 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 893 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15

102250 "ACE" 1550

	Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr
				20					25					30		
	Asn	Ala	Val	Tyr	Gly	Val	Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Lys	Glu
		35						40					45			
5	His	Ile	Ile	Pro	Glu	Lys	Asp	Tyr	Ala	Ala	Val	Ala	Phe	Asp	Lys	Lys
	50						55					60				
	Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Val	Ser	Asp	Lys	Ala	Gln	Arg
	65					70					75					80
10	Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg
					85					90					95	
	Leu	Ile	Glu	Ala	Leu	Gly	Phe	Lys	Val	Leu	Glu	Leu	Glu	Gly	Tyr	Glu
				100					105					110		
	Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Arg	Ala	Ala	Arg	Phe	Leu
			115					120					125			
15	Met	Arg	Phe	Ser	Leu	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val
	130						135					140				
	Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu
	145					150					155					160
20	Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro
					165					170					175	
	His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Asp	Ile	Asp	Asn
				180					185					190		
	Ile	Pro	Asp	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu
			195					200					205			
25	Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Tyr	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu
	210						215					220				
	Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile
	225					230					235					240
30	Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val
					245					250					255	
	Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu
				260					265					270		
	Pro	Ile	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
			275					280					285			
35	Leu	Tyr	Glu	Glu	Ala	Glu	Pro	Thr	Gly	Tyr	Glu	Ile	Val	Lys	Asp	His
	290						295					300				

30

Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala	1	5	10	15
Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr	20	25	30	
Asn	Ala	Val	Tyr	Asp	Val	Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Lys	Glu	35	40	45	
His	Ile	Ile	Pro	Glu	Lys	Asp	Tyr	Ala	Ala	Val	Ala	Phe	Asp	Lys	Lys	50	55	60	
Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Val	Ser	Asp	Lys	Ala	Gln	Arg	65	70	75	80
Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg	85	90	95	
Leu	Ile	Glu	Ala	Leu	Gly	Phe	Lys	Val	Leu	Glu	Leu	Glu	Gly	Tyr	Glu	100	105	110	
Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Arg	Ala	Ala	Arg	Phe	Leu	115	120	125	
Met	Arg	Phe	Ser	Leu	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val	130	135	140	
Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu	145	150	155	160
Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro	165	170	175	
His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Asp	Ile	Asp	Asn	180	185	190	
Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu	195	200	205	

35

35

35 Lys Ile Val Gly Gln Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val

[illegible]

His Leu Ser Gly Asp Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile
405 410 415

Asp Val His Thr Leu Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu
420 425 430

5 Glu Val Asn Glu Glu Met Arg Arg Val Gly Lys Met Val Asn Phe Ser
435 440 445

Ile Ile Tyr Gly Val Thr Pro Tyr Gly Leu Ser Val Arg Leu Asn Ile
450 455 460

10 Pro Val Lys Glu Ala Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr
465 470 475 480

Pro Lys Val Arg Ser Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu
485 490 495

Lys Gly Tyr Val Arg Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln
500 505 510

15 Leu Met Ala Arg Asp Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala
515 520 525

Ile Asn Thr Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala
530 535 540

20 Met Ile Asp Ile Asp Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg
545 550 555 560

Met Ile Ile Gln Val His Asp Glu Leu Val Phe Glu Val Pro Asp Glu
565 570 575

Glu Lys Glu Glu Leu Val Asp Leu Val Lys Asn Lys Met Thr Asn Val
580 585 590

25 Val Lys Leu Ser Val Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser
595 600 605

Trp Ser
610

(2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /note= "'Xaa' is any amino acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Arg Xaa Xaa Xaa Lys Xaa Xaa Xaa Phe Xaa Xaa Xaa Tyr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 Arg Arg Ser Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

25 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

Arg Asp Asn Ala Lys Thr Phe Ile Tyr Gly Phe Leu Tyr Gly
1 5 10

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Gln Ala Ala Lys Ala Ile Thr Phe Gly Ile Leu Tyr Gly
1 5 10

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:18:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Ser Phe Ala Leu Asp Leu Glu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Val Phe Ala Phe Asp Thr Glu Thr Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

31

5

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

10

Phe Leu Phe Asp Gly Thr

1 5

15

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

20

Leu Leu Val Asp Gly His

1 5

25

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

30

Ser Leu Ile Thr Gly Asp Lys Asp Met Leu

1	5	10
---	---	----

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAGGCCAGG GCTGTGCCGG CAAAGAGAAA TAGTC

35

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGCATATC CTTGGCGCCG GTTATTATGA AAATC

35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CACCAGACGG GTACCGCCAC TGGCAGGTTG

30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTTCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TATAGAGTAG TTAACCATCT TTCCAACCCG TTGCATTTCT TCGAACAC

48

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

48

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAAGAGGCAC AGAGAGTTTC ACC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTATATTATA GAGGAGTTAA CCATCTTTCC

30

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 AAGATGGTTA ACTTCTCTAT AATATACGG

29

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TATAGAGTAG TTAACCATCT TTCCAACCCG GTACATGTCT TCGTTCAC

48

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TATAGAGTAG TTAACCATCT TTCCAACCCG CAACATGTCT TCGTTCAC

48

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTGCCCGCC CGATGCATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTGCCCGCC CGCTTCATGA GGGGGTCCAC

30

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGCCGCC CTGTACATCA GGGGGTC

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

15 GTATATTATA GAGGTGTTAA CCATCTTTCC

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGGAGACCGG AATTCTCCTT CATTAATTCC TATA

34

25 (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

49

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACGAACATTC TACAAGTTAC

20

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTCAGAGAA ACTGACCTGT

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATAAATGCC AAACATGTTG T

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCTCTCAGG ATTCCTCCA

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTGAGAC CTCTGTGTCC

20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTCAGAAGA AACAGTGATG GT

22

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGGAGTCGC AAGCTGAACT AGC

23

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCCTGAGTGA CAGAGTGAGA ACC

23

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

15 CCCACTAGGT TGTAAGCTCC ATGA

24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TACTATGTGC CAGGCTCTGT CCTA

24

25 (2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

30

T02290" cctt6360

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTCATGAAG GTGACAGTTC

20

(2) INFORMATION FOR SEQ ID NO:60:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTGTTGTTGA CCTATTGCAT

20

(2) INFORMATION FOR SEQ ID NO:61:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATCTCTGTTC CCTCCCTGTT

20

(2) INFORMATION FOR SEQ ID NO:62:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTATTGGCC TTGAAGGTAG

20

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCCCGTGTT GGAACCATGA CTG

23

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TACATAGCGA GACTCCATCT CCC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TTTATGCGAG CGTATGGATA

20

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CACCACCATT GATCTGGAAG

20

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCAACCACAC TGGGAA

16

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACAGTTGCC CACGGT

16

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATGAAATGC TGACTGGGTA

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

15 TCAATTTATG TGCAGCCAAT

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATAGCGAGA CTCCATCTCC

20

25 (2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGGAGAGGGC AAAGATCGAT

20

(2) INFORMATION FOR SEQ ID NO:73:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AACACTAGTG ACATTATTTT CA

22

(2) INFORMATION FOR SEQ ID NO:74:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGCTAGGCCT GAAGGCTTCT

20

(2) INFORMATION FOR SEQ ID NO:75:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCCTAGTGGA TGATAAGAAT AATC

24

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGACAGATGA TAAATACATA GGATGGATGG

30

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTCTCTTACA ACACTGCCCC

20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATTTGGATGG CTTGACAGAG

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ACATTCTAAG ACTTTCCCAA T

21

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AGAGCATGCA CCCTGAATTG

20

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGAACCATG CGATACGACT

20

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CATTCCTAGA TGGGTAAAGC

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

15 GCTTAGTCAT ACGAGCGG

18

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCCACAGCCA TGTAACCC

18

25 (2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

30

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CCCCGGAGCA AGTTCA

16

(2) INFORMATION FOR SEQ ID NO:86:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

10 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGCCCAAAG CCAGATTA

18

(2) INFORMATION FOR SEQ ID NO:87:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATATGTGAGT CAATTCCCCA AG

22

(2) INFORMATION FOR SEQ ID NO:88:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTATTAGTC AATGTTCTCC AG

22

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAGCTGCCCT AGTCAGCAC

19

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20 GCTTCCGAGT GCAGGTCACA

20

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATTCTGGGCG CACAAGAGTG A

21

5

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

20

15

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

33